

SEARCH REQUEST FORM

Access DB#

27616

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

FOR OFFICIAL USE ONLY

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: _____	NA Sequence (F) _____	STN _____
Searcher Phone #: _____	AA Sequence (F) _____	Dialog _____
Searcher Location: _____	Structure (F) _____	Questel/Orbit _____
Date Searcher Picked Up: 11/16/02	Bibliographic _____	Dr. Link _____
Date Completed: 11/17/02	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems 04
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

PTO-1590 (1-2000)

Thu Nov 16 15:44:22 2000

QY 1 PROQ6 6
 11111
 DB 14 pepq9 19

RESULT 12

XX 73845
 XX 73845 standard; protein: 127 AA.

XX V73845.

XX 14-MAR-2000 (first entry)

XX Human prostate tumor EST fragment derived protein 132.

XX Pancreatic tumor; EST: expressed sequence tag; human; cytosolic.

XX treatment.

XX Homo sapiens.

XX DE9820190-AL.

XX 04-NOV-1995.

XX 28-APR-1998: 9808-1000190.

XX 28-APR-1998: 9808-1000190.

XX (METS-) METVAIN CES GENEPOSITIVE MMH.

XX Rosenthal A, Specht T, Hiltmann B, Schmitt A, Platsky C, Dahl E;

XX WFI: 1999-62186/94.

XX N-7508; 222888.

XX New human nucleic acid sequences from pancreatic tumors, and related

XX proteins.

XX CLAIM 23: Page 331: 502pp; German.

XX This invention describes novel polypeptides and their encoding nucleic

XX acid derived from human pancreatic tumor tissue which have cytostatic

XX activity. The sequences are also useful in producing antibodies against

XX protein fragments encoded by the human pancreatic tumor cDNA library

XX derived expressed sequence tag (EST) sequences represented in

XX CC 222888-23014.

XX Sequence 127 AA;

XX

XX

XX

XX

XX

XX

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XX

XX

XX

XX

KW bioticeid: antiparasitic agent; ruminant growth promoter;
 KW bioticeid: receptor agonist; antagonist; biomass.

XX streptococcus griseus.

XX W200000613-AL.

XX 06-JAN-2000.

XX 25-JUN-1995: 9960-W000195.

XX 26-JUN-1995: 98P-0202148.

XX (GTE-) RITINSINIV LEIDEN.

XX (NME-) NEDERLANDSE OEG NEDERLANDSE OEG.

XX Van Wezel JP, Kral B, Luiten RM;

XX WFI: 2000-12289/73.

XX N-7508; 249272; 449278.

XX Reducing branching and enhancing fragmentation in filamentous

XX microorganisms used to improve their liquid culturing properties.

XX Disclosure: P19 5: 6pp; English.

XX The present sequence is S. griseus Sga protein. Sga reduce branching

XX and fragment separation and enhances fragmentation of mycelium in liquid

XX culture resulting in improved with sga gene-containing plasmid to enhance

XX the production of secondary metabolites such as, antibiotics, antitumor

XX agents, immunosuppressive agents, antiparasitic agents, antiparasitic agents

XX mutant growth promoters, bioticeid: receptor agonists and

XX antagonists and biomass.

XX Sequence 135 AA;

XX

XX

XX

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XX

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XX

XX

XX

XX

XX

XX

XX

XX

bioticeid: antiparasitic agent; ruminant growth promoter;
 bioticeid: receptor agonist; antagonist; biomass.

streptococcus griseus.

W200000613-AL.

06-JAN-2000.

25-JUN-1995: 9960-W000195.

26-JUN-1995: 98P-0202148.

(GTE-) RITINSINIV LEIDEN.

(NME-) NEDERLANDSE OEG NEDERLANDSE OEG.

Van Wezel JP, Kral B, Luiten RM;

WFI: 2000-12289/73.

N-7508; 249272; 449278.

Reducing branching and enhancing fragmentation in filamentous

microorganisms used to improve their liquid culturing properties.

Disclosure: P19 5: 6pp; English.

The present sequence is S. griseus Sga protein. Sga reduce branching

and fragment separation and enhances fragmentation of mycelium in liquid

culture resulting in improved with sga gene-containing plasmid to enhance

the production of secondary metabolites such as, antibiotics, antitumor

agents, immunosuppressive agents, antiparasitic agents, antiparasitic agents

mutant growth promoters, bioticeid: receptor agonists and

antagonists and biomass.

Sequence 135 AA;

GenCode version 4.5
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ON protein - protein search, using sw model

Run on: November 16, 2000, 15:38:09 / Search time 12.25 seconds

(without alignments)
6.213 million cell updates/sec

Title: US-09-308-237D-1

Sequence: 1 PRODIG 6

Scoring table: RSCORING2

Gapex 10.0, Gapex 0.5

Searched: 164579 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Maximum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum MATCH 10%

Listing first 45 summaries

Database: Israel Protein A.A.*

1: /c0n2.5/protein/2/isa/2A.COMB.pep.*

2: /c0n2.5/protein/2/isa/2A.COMB.pep.*

3: /c0n2.5/protein/2/isa/2A.COMB.pep.*

4: /c0n2.5/protein/2/isa/2A.COMB.pep.*

5: /c0n2.5/protein/2/isa/2A.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB ID	Description
1	31	88.6	374	1	Sequence 11, Appl
2	31	88.6	374	1	Sequence 11, Appl
3	31	88.6	374	1	Sequence 11, Appl
4	31	88.6	374	1	Sequence 11, Appl
5	31	88.6	374	1	Sequence 11, Appl
6	29	82.9	322	2	Sequence 6, Appl
7	29	82.9	322	2	Sequence 6, Appl
8	29	82.9	322	2	Sequence 6, Appl
9	29	82.9	322	2	Sequence 6, Appl
10	29	82.9	322	2	Sequence 6, Appl
11	29	82.9	322	2	Sequence 6, Appl
12	29	82.9	322	2	Sequence 6, Appl
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14	29	82.9	322	2	Sequence 6, Appl
15	29	82.9	322	2	Sequence 6, Appl
16	29	82.9	322	2	Sequence 6, Appl
17	29	82.9	322	2	Sequence 6, Appl
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23	29	82.9	322	2	Sequence 6, Appl
24	29	82.9	322	2	Sequence 6, Appl
25	29	82.9	322	2	Sequence 6, Appl
26	29	82.9	322	2	Sequence 6, Appl
27	29	82.9	322	2	Sequence 6, Appl
28	29	82.9	322	2	Sequence 6, Appl

29	28	80.0	144	2	Sequence 1, Appl
30	28	80.0	144	2	Sequence 1, Appl
31	28	80.0	144	2	Sequence 1, Appl
32	28	80.0	144	2	Sequence 1, Appl
33	28	80.0	144	2	Sequence 1, Appl
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37	28	80.0	144	2	Sequence 1, Appl
38	28	80.0	144	2	Sequence 1, Appl
39	28	80.0	144	2	Sequence 1, Appl
40	28	80.0	144	2	Sequence 1, Appl
41	28	80.0	144	2	Sequence 1, Appl
42	28	80.0	144	2	Sequence 1, Appl
43	28	80.0	144	2	Sequence 1, Appl
44	28	80.0	144	2	Sequence 1, Appl
45	28	80.0	144	2	Sequence 1, Appl

ALSUMMARIES

1	US-07-914-281-11	Sequence 11, Application US/07914281
2	US-07-914-281-11	Sequence 11, Application US/07914281
3	US-07-914-281-11	Sequence 11, Application US/07914281
4	US-07-914-281-11	Sequence 11, Application US/07914281
5	US-07-914-281-11	Sequence 11, Application US/07914281
6	US-07-914-281-11	Sequence 11, Application US/07914281
7	US-07-914-281-11	Sequence 11, Application US/07914281
8	US-07-914-281-11	Sequence 11, Application US/07914281
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16	US-07-914-281-11	Sequence 11, Application US/07914281
17	US-07-914-281-11	Sequence 11, Application US/07914281
18	US-07-914-281-11	Sequence 11, Application US/07914281
19	US-07-914-281-11	Sequence 11, Application US/07914281
20	US-07-914-281-11	Sequence 11, Application US/07914281
21	US-07-914-281-11	Sequence 11, Application US/07914281
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23	US-07-914-281-11	Sequence 11, Application US/07914281
24	US-07-914-281-11	Sequence 11, Application US/07914281
25	US-07-914-281-11	Sequence 11, Application US/07914281
26	US-07-914-281-11	Sequence 11, Application US/07914281
27	US-07-914-281-11	Sequence 11, Application US/07914281
28	US-07-914-281-11	Sequence 11, Application US/07914281

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us-09-308-237b-1.ra1

Page 2

DB 137 PTHROC 342

RESULT 2

US-08-593-0584-11

Sequence 11, Application US/08/93246

Patent No. 5595900

APPLICANT: OHLON, SPYNAK, MCLELLAND, MATER & NEIRSTADT

ATTORNEY/AGENT INFORMATION:

NAME: LAVOLETTE, JEAN-PAUL M. P.

REFERENCE/DOCKET NUMBER: 1363-060-55

TELEPHONE: (703)321-4300

TELEX: 248855 OPAAT US

INSPIRATION FOR SEQ ID NO: 11:

SEQUENCE: 374 amino acids

LENGTH: 374 amino acids

TYPE: amino acid

MOLECULE TYPE: protein

US-08-593-0584-11

Query Match

88.4% Score 31: DB 1: Length 374:

Best Local Similarity: 83.3%: Pred. No. 1.3e+02:

Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

DB 137 PTHROC 342

RESULT 3

US-08-593-0584-11

Sequence 11, Application US/08/93246

Patent No. 5595900

APPLICANT: OHLON, SPYNAK, MCLELLAND, MATER & NEIRSTADT

ATTORNEY/AGENT INFORMATION:

NAME: LAVOLETTE, JEAN-PAUL M. P.

REFERENCE/DOCKET NUMBER: 1363-060-55

TELEPHONE: (703)321-4300

TELEX: 248855 OPAAT US

INSPIRATION FOR SEQ ID NO: 11:

SEQUENCE: 374 amino acids

LENGTH: 374 amino acids

TYPE: amino acid

MOLECULE TYPE: protein

US-08-593-0584-11

Query Match

88.4% Score 31: DB 1: Length 374:

Best Local Similarity: 83.3%: Pred. No. 1.3e+02:

Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

DB 137 PTHROC 342

RESULT 4

US-08-593-0584-11

Sequence 11, Application US/08/93246

Patent No. 5595900

APPLICANT: OHLON, SPYNAK, MCLELLAND, MATER & NEIRSTADT

ATTORNEY/AGENT INFORMATION:

NAME: LAVOLETTE, JEAN-PAUL M. P.

REFERENCE/DOCKET NUMBER: 1363-060-55

TELEPHONE: (703)321-4300

TELEX: 248855 OPAAT US

INSPIRATION FOR SEQ ID NO: 11:

SEQUENCE: 374 amino acids

LENGTH: 374 amino acids

TYPE: amino acid

MOLECULE TYPE: protein

US-08-593-0584-11

Query Match

88.4% Score 31: DB 1: Length 374:

Best Local Similarity: 83.3%: Pred. No. 1.3e+02:

Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

DB 137 PTHROC 342

RESULT 5

US-08-593-0584-11

CORRESPONDENCE ADDRESS:

ADDRESS: OHLON, SPYNAK, MCLELLAND, MATER & NEIRSTADT, P. C.

1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington

STATE: Virginia

ZIP: 22202

COMPUTER READABLE FORM:

OPERATING SYSTEM: IBM PC compatible

CURRENT APPLICATION DATA: release #1.0, Version #1.25

APPLICATION NUMBER: US/08/93246

US-08-593-0584-11

Query Match

88.4% Score 31: DB 1: Length 374:

Best Local Similarity: 83.3%: Pred. No. 1.3e+02:

Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

DB 137 PTHROC 342

RESULT 6

US-08-593-0584-11

Sequence 11, Application US/08/93246

Patent No. 5595900

APPLICANT: OHLON, SPYNAK, MCLELLAND, MATER & NEIRSTADT

ATTORNEY/AGENT INFORMATION:

NAME: LAVOLETTE, JEAN-PAUL M. P.

REFERENCE/DOCKET NUMBER: 1363-060-55

TELEPHONE: (703)321-4300

TELEX: 248855 OPAAT US

INSPIRATION FOR SEQ ID NO: 11:

SEQUENCE: 374 amino acids

LENGTH: 374 amino acids

TYPE: amino acid

MOLECULE TYPE: protein

US-08-593-0584-11

Query Match

88.4% Score 31: DB 1: Length 374:

Best Local Similarity: 83.3%: Pred. No. 1.3e+02:

Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

DB 137 PTHROC 342

RESULT 7

US-08-593-0584-11

Sequence 11, Application US/08/93246

Patent No. 5595900

APPLICANT: OHLON, SPYNAK, MCLELLAND, MATER & NEIRSTADT

ATTORNEY/AGENT INFORMATION:

NAME: LAVOLETTE, JEAN-PAUL M. P.

REFERENCE/DOCKET NUMBER: 1363-060-55

TELEPHONE: (703)321-4300

TELEX: 248855 OPAAT US

INSPIRATION FOR SEQ ID NO: 11:

SEQUENCE: 374 amino acids

LENGTH: 374 amino acids

TYPE: amino acid

MOLECULE TYPE: protein

US-08-593-0584-11

Query Match

88.4% Score 31: DB 1: Length 374:

Best Local Similarity: 83.3%: Pred. No. 1.3e+02:

Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

DB 137 PTHROC 342

RESULT 8

US-08-593-0584-11

Sequence 11, Application US/08/93246

Patent No. 5595900

APPLICANT: OHLON, SPYNAK, MCLELLAND, MATER & NEIRSTADT

ATTORNEY/AGENT INFORMATION:

NAME: LAVOLETTE, JEAN-PAUL M. P.

REFERENCE/DOCKET NUMBER: 1363-060-55

TELEPHONE: (703)321-4300

TELEX: 248855 OPAAT US

INSPIRATION FOR SEQ ID NO: 11:

SEQUENCE: 374 amino acids

LENGTH: 374 amino acids

TYPE: amino acid

MOLECULE TYPE: protein

US-08-593-0584-11

Query Match

88.4% Score 31: DB 1: Length 374:

Best Local Similarity: 83.3%: Pred. No. 1.3e+02:

Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

DB 137 PTHROC 342

APPLICATION NUMBER: US 08/220,433
 FILING DATE: 30-Mar-1994
 APPLICATION NUMBER: US 07/914,281
 ATTORNEY/AGENT INFORMATION:
 NAME: Lavalley, Jean-Paul M. P.
 REFERENCE/DOCKET NUMBER: 2353-060-95
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703/162-2347
 TELEFAX: 703/162-2347
 TELEX: 248953 OPAK UR
 INVENTION FOR SEQ ID NO: 11:
 SUBSTANCE: amino acid
 LENGTH: 374 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 US-08-696-731-11

Query Match 82.94; Score 31; DB 2; Length 374;
 Best Local Similarity 83.34; Pred No. 24+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 PROPG 6
 Db 137 PROPG 142

RESULT 5
 US-08-319-704-6
 Sequence 6, Application US/08319704
 GENERAL INFORMATION:
 APPLICANT: Hoffman, Stephen L.
 APPLICANT: Hoffman, Stephen L.
 APPLICANT: Hoffman, Stephen L.
 TITLE OF INVENTION: Proteinase 11
 TITLE OF INVENTION: Proteinase 11
 NUMBER OF SOURCES: 11
 CORRESPONDENCE ADDRESS:
 STREET: Bldg J, 7-12, 8901 Wisconsin Avenue
 CITY: Bethesda
 STATE: Md 20814
 COUNTRY: US
 ZIP: 20889-5606
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA: Version 41.25
 APPLICATION NUMBER: US/08/319 704
 CLASSIFICATION: 424-1394
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoffman, Stephen L.
 REFERENCE/DOCKET NUMBER: 75,206
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301/295-1022
 TELEFAX: 301/295-1022
 INFORMATION FOR SEQ ID NO: 6:
 SUBSTANCE: amino acid
 LENGTH: 163 amino acids
 TYPE: amino acid
 MOLECULE TYPE: peptide
 US-08-319-704-6

Query Match 82.94; Score 29; DB 2; Length 162;
 Best Local Similarity 83.34; Pred No. 12+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 PROPG 6
 Db 146 PROPG 151

RESULT 6
 US-08-651-819A-3
 Sequence 6, Application US/08651819A
 GENERAL INFORMATION:
 APPLICANT: Hale, Cynthia A.
 APPLICANT: Hale, Cynthia A.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING
 NUMBER OF SOURCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESS: 320 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94104
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA: Version 41.30
 APPLICATION NUMBER: US/08/651,819A
 FILING DATE: 510
 ATTORNEY/AGENT INFORMATION:
 NAME: Carroll, Peter G.
 REFERENCE/DOCKET NUMBER: CASE 02249
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/763-1310
 INFORMATION FOR SEQ ID NO: 3:
 SUBSTANCE CHARACTERISTICS:
 TYPE: amino acid
 STANDARDS: not relevant
 MOLECULE TYPE: protein
 US-08-651-819A-3

Query Match 82.94; Score 29; DB 2; Length 377;
 Best Local Similarity 100.00; Pred No. 24+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 PROPG 5
 Db 123 PROPG 127

RESULT 7
 US-09-118-319-6
 Sequence 6, Application US/091819
 GENERAL INFORMATION:
 APPLICANT: Li, Xin-Liang
 APPLICANT: Li, Xin-Liang
 TITLE OF INVENTION: Orymyces Cellulase Gene and Coding Sequences
 CURRENT APPLICATION NUMBER: US/09/118-319

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Page 4

CURRENT FILING DATE: 1998-07-17
 NUMBER OF SEQ ID NOS: 0
 SOFTWARE: PatentB Ver. 2.0
 SEQ ID NO: 6
 TYPE: PAT
 US-09-118-319-6
 ORGANISM: Oryzomys sp. PC-2

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 Best Local Similarity: 82.94% Score 29; DB 3; Length 459;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PROPG 5
 11111
 Db 119 PROPG 123

RESULT 8
 US-09-071-101-2
 Sequence 2: Application US/08765931
 Patent No. 5948657
 GENERAL INFORMATION: Kyo-Tsuo
 APPLICANT: Saitama; Leonard B.
 APPLICANT: Liu, Jui-Hao
 APPLICANT: Forbush, Cecil H.
 APPLICANT: Moloney, Maurice M.
 TITLE OF INVENTION: A synthetic oligonucleotide
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS: Winner and Sullivan, P.C.
 STREET: 5370 Manhattan Circle, Suite 201
 CITY: Boulder
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80803
 COMPUTER: IBM PC compatible
 SOFTWARE: PatentB Ver. 2.0, Version 41.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/719,391
 CLASSIFICATION: 433.1996
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 1321-1-002
 HIRSHENFELD/DOCKERTY NUMBER: 93-96
 TELEPHONE: (303) 439-8080
 INVENTION FOR SEQ ID NO: 2:
 SOURCE:
 TYPE: amino acid
 LENGTH: 485 amino acids
 MOLECULE TYPE: protein
 US-08-749-351-2

Query Match
 Best Local Similarity: 82.94% Score 29; DB 2; Length 485;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 PROPG 6
 Db 331 PROPG 316

RESULT 9
 US-09-071-101-2
 Sequence 7: Application US/0867166A
 Patent No. 5951770
 GENERAL INFORMATION:
 APPLICANT: Forbush, Cecil H.
 APPLICANT: Moloney, Maurice M.
 TITLE OF INVENTION: EXPLOITATION OF THE CELLULASE COMPLEX OF
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS: Jackson, Bob
 STREET: 411 Broadway Ave., Continental Plaza, 4th
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07201
 COMPUTER: IBM PC compatible
 SOFTWARE: PatentB Ver. 2.0, Version 41.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/676,166A
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 1321-1-002
 HIRSHENFELD/DOCKERTY NUMBER: 26-742
 TELEPHONE: 201-487-5800
 INVENTION FOR SEQ ID NO: 7:
 SOURCE:
 TYPE: amino acid
 LENGTH: 516 amino acids
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: P. chrysosporium
 US-08-676-166A-7

Query Match
 Best Local Similarity: 82.94% Score 29; DB 2; Length 516;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 PROPG 6
 Db 474 PROPG 479

RESULT 10
 US-09-071-101-2
 Patent No. 6015603
 GENERAL INFORMATION:
 APPLICANT: Jaspers, Stephen B.
 TITLE OF INVENTION: HUMAN PHOSPHOMONOCYTES 4
 CORRESPONDENCE ADDRESS:
 ADDRESS: Zymogenetics, Inc.
 STREET: 1201 Baylake Avenue East
 STATE: WA
 COUNTRY: USA
 ZIP: 98102


```

13      12. 15934733
14      13. 15934733
15      14. Application US/08/42753
16      15. 15934733
17      16. Patent No. 5661278
18      17. GENERAL INFORMATION:
19      18. INVENTOR: KORDON, Gordon G.
20      19. APPLICANT: YAO, Kwok-Hing
21      20. TITLE OF INVENTION: 4.1.5 delta Compositions
22      21. NUMBER OF PAGES: 4
23      22. CORRESPONDENCE ADDRESS: Teatime, Inc.
24      23. ADDRESS: 81 Cambridgepark Drive
25      24. CITY: Cambridge
26      25. STATE: Massachusetts
27      26. ZIP: 02140
28      27. COMPUTER READABLE FORM:
29      28. COMPUTER: IBM PC compatible
30      29. OPERATING SYSTEM: PC-DOS/MS-DOS
31      30. CURRENT APPLICATION NUMBER: 08/42753
32      31. CURRENT APPLICATION DATA: 41.0, Version #1.25
33      32. APPLICATION NUMBER: US/08/742.753
34      33. CLASSIFICATION: 514
35      34. ATTORNEY/AGENT INFORMATION:
36      35. NAME:
37      36. REGISTRATION NUMBER: 32,618
38      37. REFERENCE/DOCKET NUMBER: 5277
39      38. FILE NUMBER: 61617, 498-9260
40      39. TELEFAX: (617) 876-9851
41      40. INFORMATION FOR ANALYTICS: 4:
42      41. SEQUENCE: 763 amino acids
43      42. LENGTH: 763 amino acids
44      43. TYPE: amino acid
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MEDIUM TYPE: BLANKET
COMPUTER: IBM COMPATIBLE
CURRENT APPLICATION VERSION: 2.0
APPLICATION NUMBER: US/08/537,210A
CLASSIFICATION: 59-58P-1995
CLASSIFICATION: 59-58P-1995
ATTORNEY/AGENT INFORMATION:
NAME: MITROCK, S. LAILIE
REFERENCE/DOCKET NUMBER: 97325-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-469-8664
TELEFAX: 212-469-8690
TELEX: 6614 PENNIE
INVOICE NUMBER: 11111111
SEQUENCE CHARACTERISTICS:
LENGTH: 1064 amino acids
STRANDS: 1
MOLECULE TYPE: unknown
POLYMER: protein
NAME/KEY: Xaa N
LOCATION: 1150...2213
OTHER INFORMATION: Highly conserved ankyrin repeat
US-08-537-210A-3 region of No. 5780300ch

Query Match 83.9%, Score 29, DB 1, Length 1064;
Best Local Similarity 83.3%, Pred. No. 8, 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 PEPDGG 6

Db 706 PEPDGG 711

MISALIGN 34
US-08-537-210A-2
SEQUENCE 32, Application US/08537210A
Patent No. 5780300ch
GENERAL INFORMATION:
APPLICANT: ARCEVALA-TEASOAS, SPYRIDON
APPLICANT: Melsano, Koji
TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 115 Avenue G Deschamps
CITY: New York
COUNTRY: USA
ZIP: 10036/2711
COMMUNICABLE FORM:
MEDIUM READABLE FORM:
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,210A
CLASSIFICATION: 59-58P-1995
ATTORNEY/AGENT INFORMATION:
NAME: MITROCK, S. LAILIE
REFERENCE/DOCKET NUMBER: 97325-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-469-8664
TELEFAX: 212-469-8690
TELEX: 6614 PENNIE
INVOICE NUMBER: 11111111
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
STRANDS: 1
MOLECULE TYPE: protein

TELEFAX: 212-469-8664
TELEX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: "a" amino acid
STRANDS: 1
MOLECULE TYPE: protein
NAME/KEY: Xaa N (PAA-N)
LOCATION: 1153...2223
OTHER INFORMATION: Highly conserved ankyrin repeat
US-08-537-210A-2 region of No. 5780300ch

Query Match 83.9%, Score 29, DB 1, Length 1078;
Best Local Similarity 83.3%, Pred. No. 8, 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 PEPDGG 6

Db 710 PEPDGG 715

SEQUENCE 32, Application US/08264534
Patent No. 5688464
GENERAL INFORMATION:
APPLICANT: ARCEVALA-TEASOAS, SPYRIDON et al
APPLICANT: Melsano, Koji
TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 115 Avenue G Deschamps
CITY: New York
COUNTRY: USA
ZIP: 10036/2711
COMMUNICABLE FORM:
MEDIUM READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,534
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
FILING DATE: 05/04/97
ATTORNEY/AGENT INFORMATION:
NAME: MITROCK, S. LAILIE
REFERENCE/DOCKET NUMBER: 97325-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-469-8664/9741
TELEFAX: 212-469-8664/9741
TELEX: 6614 PENNIE
INVOICE NUMBER: 11111111
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
STRANDS: 1
MOLECULE TYPE: protein

Query Match 83.9%, Score 29, DB 1, Length 1078;
Best Local Similarity 83.3%, Pred. No. 8, 2e+02;

Thu Nov 16 15:44:23 2000

us-09-308-237b-1.rtf

Page 7

Matches 5: Consecutive 0: Mismatches 1: Indels 0: Gaps 0:

Qy 1 PROPOS 6

Db 407 PROPOS 412

Search completed: November 16, 2000, 15:36:28
Job time: 19 sec

GenScore version 4.5
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OR protein - protein search, using sw model

Run on: November 16, 2000, 15:35:10 ; Search time 38.32 seconds

(without alignments)
21,314 Million cell updates/sec

Title: US-09-308-237b-1

Perfect score: 35

Sequence: 1 EYVQC 6

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 872601 seqs, 136121714 residues

Total number of hits satisfying chosen parameters: 872601

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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27. /csm2_6/prodata/2/paa/US08.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	35	100.0	6	US-09-308-237b-1	Sequence 1, Appl
2	35	100.0	6	US-09-308-237b-1	Sequence 1, Appl
3	35	100.0	6	US-09-308-237b-1	Sequence 1, Appl
4	35	100.0	6	US-09-308-237b-1	Sequence 1, Appl
5	35	100.0	6	US-09-308-237b-1	Sequence 1, Appl
6	35	100.0	6	US-09-308-237b-1	Sequence 1, Appl

ALIGNMENTS

Result No.	Score	Match	Length	ID	Description
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2	35	100.0	6	US-09-308-237b-1	Sequence 1, Appl
3	35	100.0	6	US-09-308-237b-1	Sequence 1, Appl
4	35	100.0	6	US-09-308-237b-1	Sequence 1, Appl
5	35	100.0	6	US-09-308-237b-1	Sequence 1, Appl
6	35	100.0	6	US-09-308-237b-1	Sequence 1, Appl

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us-09-308-237b-1.rap

Page 3

Query Match 91.4% Score 32: DB 21: Length 603:
Best Local Similarity 83.3% Pred. No. 1.0e+03:
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

DB 338 PRF006 443
1 PROPG 6
11:1111

RESULT 5

PERSEQUENCE 3537.1

GENERAL INFORMATION: Application PC/MS9922517

APPLICANT INFORMATION: Dept of Columbia University, 10 the City o

APPLICANT INVENTION: Gene encoding MMR2 and Uses Thereof

FILE REFERENCE: 57497 A-CTD/JP/AL

CURRENT APPLICATION NUMBER: US/09/443/704

CURRENT FILING DATE: 1999-11-19

EXPIRATION DATE: 2009-11-19

EXPIRATION FILING DATE: 1998-09-29

EXPIRATION APPLICATION NUMBER: US/09/443/524

SOFTWARE: Patent Ver. 2.0 - beta

SEQ ID NO 1

LENGTH: 300

TYPE: nt

ORGANISM: chicken embryo

PCT-0599-22517-1

Query Match 88.6% Score 31: DB 1: Length 300:
Best Local Similarity 83.3% Pred. No. 8.1e+03:
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

DB 238 PRF006 243
1 PROPG 6
1:1111

RESULT 6

PERSEQUENCE 162.524.1

GENERAL INFORMATION: US/09162524

APPLICANT: Jansell, Thomas M.

APPLICANT INVENTION: Gene encoding MMR2 and Uses Thereof

FILE REFERENCE: 57497 A-CTD/JP/AL

CURRENT APPLICATION NUMBER: US/09/443/524

CURRENT FILING DATE: 1998-09-29

EXPIRATION DATE: 2008-09-29

EXPIRATION APPLICATION NUMBER: US/09/443/524

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 1

LENGTH: 300

TYPE: nt

ORGANISM: chicken embryo

US-09-162-524-1

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Best Local Similarity 83.3% Pred. No. 1.0e+03:
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DB 238 PRF006 243
1 PROPG 6
1:1111

RESULT 7

PERSEQUENCE 162.524.1

GENERAL INFORMATION: US/09162524

APPLICANT: Jansell, Thomas M.

APPLICANT INVENTION: Gene encoding MMR2 and Uses Thereof

FILE REFERENCE: 57497 A-CTD/JP/AL

CURRENT APPLICATION NUMBER: US/09/443/524

CURRENT FILING DATE: 1998-09-29

EXPIRATION DATE: 2008-09-29

EXPIRATION APPLICATION NUMBER: US/09/443/524

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 1

LENGTH: 300

TYPE: nt

ORGANISM: chicken embryo

US-09-162-524-1

APPLICANT: Odeil, Jean
APPLICANT INVENTION: MMR-Related Transcription Factors
APPLICANT: Weng, Jude
TITLE OF INVENTION: MMR-Related Transcription Factors

CURRENT APPLICATION NUMBER: US/09/443/704
CURRENT FILING DATE: 1999-11-19
EXPIRATION DATE: 2009-11-19
EXPIRATION FILING DATE: 1998-09-29
EXPIRATION APPLICATION NUMBER: US/09/443/524
SOFTWARE: Microsoft Office 97

SEQ ID NO 1

LENGTH: 302

TYPE: nt

ORGANISM: max

US-09-443-704-12

Query Match 88.6% Score 31: DB 18: Length 300:
Best Local Similarity 83.3% Pred. No. 8.1e+03:
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

DB 220 PRF006 225
1 PROPG 6
1:1111

RESULT 8

PERSEQUENCE 162.524.1

GENERAL INFORMATION: US/08231489

APPLICANT: Jansell, Thomas M.

APPLICANT INVENTION: Gene encoding MMR2 and Uses Thereof

FILE REFERENCE: 57497 A-CTD/JP/AL

CURRENT APPLICATION NUMBER: US/09/443/704

CURRENT FILING DATE: 1999-11-19

EXPIRATION DATE: 2009-11-19

EXPIRATION APPLICATION NUMBER: US/09/443/524

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 1

LENGTH: 300

TYPE: nt

ORGANISM: chicken embryo

US-09-162-524-1

Query Match 88.6% Score 31: DB 18: Length 300:
Best Local Similarity 83.3% Pred. No. 8.1e+03:
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

DB 220 PRF006 225
1 PROPG 6
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RESULT 9

PERSEQUENCE 162.524.1

GENERAL INFORMATION: US/08231489

APPLICANT: Jansell, Thomas M.

APPLICANT INVENTION: Gene encoding MMR2 and Uses Thereof

FILE REFERENCE: 57497 A-CTD/JP/AL

CURRENT APPLICATION NUMBER: US/09/443/704

CURRENT FILING DATE: 1999-11-19

EXPIRATION DATE: 2009-11-19

EXPIRATION APPLICATION NUMBER: US/09/443/524

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 1

LENGTH: 300

TYPE: nt

ORGANISM: chicken embryo

US-09-162-524-1

Query Match 88.6% Score 31: DB 18: Length 300:
Best Local Similarity 83.3% Pred. No. 8.1e+03:
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

DB 220 PRF006 225
1 PROPG 6
1:1111

RESULT 10

PERSEQUENCE 162.524.1

GENERAL INFORMATION: US/08231489

APPLICANT: Jansell, Thomas M.

APPLICANT INVENTION: Gene encoding MMR2 and Uses Thereof

FILE REFERENCE: 57497 A-CTD/JP/AL

CURRENT APPLICATION NUMBER: US/09/443/704

CURRENT FILING DATE: 1999-11-19

EXPIRATION DATE: 2009-11-19

EXPIRATION APPLICATION NUMBER: US/09/443/524

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 1

LENGTH: 300

TYPE: nt

ORGANISM: chicken embryo

US-09-162-524-1

SEQ ID NO 2970
 LENGTH: 58
 TYPE: PRT HUMAN
 ORGANISM: HUMAN
 US-60-177-571-2970

Query Match
 Best Local Similarity 83.3% Score 30: DB 21: Length 58:
 Matches 5: Conservative 0: Mismatches 1: Indels 0: Gaps 0:
 1 PROPG 6
 16 PTDG 21

RESULT 13
 US-60-177-571-2820
 : Sequence 2820, Application US/6017571
 : GENERAL INFORMATION: VITAE
 : TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 : TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 : FILE REFERENCE: CIL00014
 : CURRENT APPLICATION NUMBER: US/60/177, 571
 : CURRENT FILING DATE: 1995-12-09
 : SOFTWARE: FASTED FOR Windows Version 4.0
 : SEQ ID NO 2820
 : LENGTH: 58
 : TYPE: PRT
 : ORGANISM: HUMAN
 US-60-177-571-6820

Query Match
 Best Local Similarity 83.3% Score 30: DB 21: Length 71:
 Matches 5: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

DB 34 PTDG 39

RESULT 14
 US-60-160-203-4845
 : Sequence 4845, Application US/60160203
 : GENERAL INFORMATION: VITAE
 : APPLICANT: BOWALL, VITAE
 : TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 : TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 : FILE REFERENCE: CIL00014
 : CURRENT APPLICATION NUMBER: US/60/160, 203
 : CURRENT FILING DATE: 1995-10-13
 : SOFTWARE: FASTED FOR Windows Version 4.0
 : SEQ ID NO 4845
 : LENGTH: 76
 : TYPE: PRT
 : ORGANISM: HUMAN
 US-60-160-203-4845

Query Match
 Best Local Similarity 83.3% Score 30: DB 21: Length 76:
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 34 PTDG 39

RESULT 15
 US-60-169-840-6635
 : Sequence 6635, Application US/60169840
 : GENERAL INFORMATION: VITAE
 : APPLICANT: BOWALL, VITAE
 : TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 : TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 : FILE REFERENCE: CIL00014
 : CURRENT APPLICATION NUMBER: US/60/169, 840
 : CURRENT FILING DATE: 1995-12-09
 : SOFTWARE: FASTED FOR Windows Version 4.0
 : SEQ ID NO 6635
 : LENGTH: 76
 : TYPE: PRT
 : ORGANISM: Human
 US-60-169-840-6635

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 1 PROPG 6
 34 PTDG 39

Search completed: November 16, 2000, 15:37:46
 Job name: 39 sec

Thu Nov 16 15:44:23 2000

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Page 6

Genome version 4.5
Copyright (c) 1993-2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2000, 15:36:10 : Search time 13.66 Seconds
(without alignments)

28,288 Million cell updates/sec

Title: us-09-308-237b-1

Score: 35

Sequence: 1 PTC006 6

Scoring table: BL081462

Gap: 10.0, Gapext: 0.5

Search: 18216 seqs, 63160319 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 2000000000

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Matching Method 45 summary

Database:

1: ptc1
2: ptc2
3: ptc3
4: ptc4

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the alignment printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	100	573	2	JC4335	anti-mullerian hor
2	32	91.4	792	2	anti-mullerian hor
3	32	91.4	792	2	anti-mullerian hor
4	31	88.6	557	2	anti-mullerian hor
5	31	88.6	557	2	anti-mullerian hor
6	31	88.6	557	2	anti-mullerian hor
7	31	88.6	557	2	anti-mullerian hor
8	31	88.6	557	2	anti-mullerian hor
9	30	85.7	298	2	anti-mullerian hor
10	30	85.7	298	2	anti-mullerian hor
11	30	85.7	298	2	anti-mullerian hor
12	30	85.7	298	2	anti-mullerian hor
13	30	85.7	298	2	anti-mullerian hor
14	30	85.7	298	2	anti-mullerian hor
15	30	85.7	298	2	anti-mullerian hor
16	30	85.7	298	2	anti-mullerian hor
17	30	85.7	298	2	anti-mullerian hor
18	30	85.7	298	2	anti-mullerian hor
19	30	85.7	298	2	anti-mullerian hor
20	30	85.7	298	2	anti-mullerian hor
21	30	85.7	298	2	anti-mullerian hor
22	29	82.9	460	2	anti-mullerian hor
23	29	82.9	460	2	anti-mullerian hor
24	29	82.9	460	2	anti-mullerian hor
25	29	82.9	460	2	anti-mullerian hor
26	29	82.9	460	2	anti-mullerian hor
27	29	82.9	460	2	anti-mullerian hor
28	29	82.9	460	2	anti-mullerian hor
29	29	82.9	460	2	anti-mullerian hor
30	29	82.9	460	2	anti-mullerian hor

ALIGNMENTS

RESULT 1

anti-mullerian hormone type II receptor precursor - human

C:Species: Homo sapiens (human) revision 08-Feb-1996 <ext> change 04-Mar-2000

C:Accession: J04335 <seq> revision 08-Feb-1996 <ext> change 04-Mar-2000

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C:Accession: J04335 <seq> revision 08-Feb-1996 <ext> change 04-Mar-2000

C:Accession: J04335 <seq> revision 08-Feb-1996 <ext> change 04-Mar-2000

A: *Reagents*: 1-7.9. <T/7>
A: *Cross-references*: CH:AN002120; CH:AE002160; PIDN:AAF9354.1; P.D: g71905
A: *Experimental source*: strain M19g (Mori)
C: *Cell lines*
A: *Gene*: TC0512

Query Match 91.4%; Score 32; DB 2; length 792;
Best Local Similarity 83.3%; Pred No 1e+03.

QY 1 PROPOC 6
11:111

PROB-3
 Probable omegs analog - Chlamydia trachomatis (serotype D, strain MW/3/Cx)
 C/Species: Chlamydia trachomatis
 C/Accession: U01353
 C/Sequence: evolution_13-Sep-1986 *tax.Chlamy 08-Oct-1999
 R/S: Stephens, R. S., Kalam, S., Lammel, C. J., Fan, J., Meehan, R., Award, L., Mitchell, R. M.
 A/Title: Complete sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
 A/Accession number: AF1570
 A/Version: 99090809
 A/Status: preliminary
 A/Accession type: DNA
 A/Accession type: DNA
 A/Accession type: DNA
 A/Cross-references: gb:AF001297; gb:AF001273; MF:9338646; PDB:AC67034.1; PDB:9312065
 A/Original source: serotype D, strain MW-3/Cx
 A/Date: year

```

Query Match          91.4%   Score 32;   DR 2;   Length 792;
Post Local Similarity 83.3%   P-Val. No. 1e+02;
Matches      5;   Conservative      1;   Mismatches      0;   Indels      0;   Gaps      0;
DB          1   PROTEIN 6
          1111111
DB      692   PROTEIN 697

```

[illegible][illegible]

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RED>
A:Cross-references: EMBL:U73730; NID:g967196; PIDD:MG50189.1; PTD:g9672197
C:Gene(s): CDB:
C:Gene: CDB:PU75
A:Cross-references: CDB:131644; OMTM:136615
C:Map position: 19n13.1-19n13.2

Client Material

Matches 5; Con

DB	137	PRIMED	142
REVIEW	5		
SL1627			
probable anti-müllerian hormone receptor - rat			
Crisicova, Ratusa norvegicus (Norway rat)			
Clackson, SL1627	Sequence,Nov-13-Jan-1995	142x,Chingme	24-Sep-1999
Risgaard, M.; van Halbeek, M.J.L.; Post, P.J.C.M.; Koopstra			
van Halbeek, M.J.L.; Post, P.J.C.M.; van der Stoep, P.J.C.M.; Koopstra			
Article A novel member of the transmembrane serine/threonine kinase receptor family			
Accession number: SL1627			
Status: preliminary			
MD5:9161972			

Query Match 88.6% Score 31.0n 2. Length 87n

	0:	Caps	0:
	U:	Indels	0:
A:ASCHS	U:	Indels	0:
1	6		
11017			
Ob	367	PROM	372
RESULT			
6			
bulletin-inhibiting substance type II receptor - mouse			
Species: Mus musculus (house mouse)			
Accession: U01982 sequence revision 07-Nov-1997 text change 04-Mar-2000			

[illegible]

Best Local Similarity 08.68; Score 31; DB 2; Length 568
63.38; Pred. NO. 1.1e+02;

us-09-308-237b-1.rpr

AAccession: Z08950
AStatus: preliminary translated from cDNA/EST/DBST
ACredentials: 1-7262 (CCKB)
ACrossReferences: BHLAB01560; EFIN:BA034927.1
ACrossSpecies: young adult mouse
ACrossSpeciesReference: young adult mouse
ADisease: TUG1
ASynonyms: Ca^v1.2; voltage-dependent sodium channel protein alpha-1 chain
CAcrossReferences: calcium binding; calcium channel
Query Match 85.7% Length 2262;
Similarity 83.7% Pvald no 7.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0
OY 1 PROPOSED 6
|||||
db_1839 PROPOSED 1844

Search completed: November 16, 2000, 15:37:05
Job time: 55 sec

PT	DOMAIN	509	573	(CYTOPLASMIC (POTENTIAL). B X TANDEM REPEATS, SER/THR-RICH
PT	DOMAIN	17	230	
PT	DOMAIN	17	43	
PT	DOMAIN	17	1	

F1	REPEAT	44	70	4.
F2	REPEAT	71	97	3.
F3	REPEAT	96	141	2.
F4	REPEAT	152	178	5.
F5	REPEAT	179	205	7 (NEAR PERFECT).
F6	REPEAT	206	230	9
F7	REPEAT	230	256	10
F8	DOMAIN	365	425	BE-LIKE 1.
F9	DOMAIN	425	462	BE-LIKE 2.
F10	DOMAIN	462	495	BE-LIKE 3.
F11	DISJULFD	237	248	BY SIMILARITY.
F12	DISJULFD	248	268	BY SIMILARITY.
F13	DISJULFD	256	272	BY SIMILARITY.
F14	DISJULFD	389	402	BY SIMILARITY.
F15	DISJULFD	394	408	BY SIMILARITY.
F16	DISJULFD	429	441	BY SIMILARITY.
F17	DISJULFD	433	451	BY SIMILARITY.
F18	DISJULFD	453	466	BY SIMILARITY.
F19	DISJULFD	466	482	BY SIMILARITY.
F20	CARBOHD	326	316	N-LINKED (GLC/MC).
F21	CARBOHD	326	316	N-LINKED (GLC/MC).
F22	CARBOHD	337	357	N-LINKED (GLC/MC).
F23	CARBOHD	387	357	N-LINKED (GLC/MC).
F24	CARBOHD	573	581	N-LINKED (GLC/MC).
F25	CARBOHD	581	590	N-LINKED (GLC/MC).
F26	CARBOHD	590	600	N-LINKED (GLC/MC).
F27	CARBOHD	600	610	N-LINKED (GLC/MC).
F28	CARBOHD	610	620	N-LINKED (GLC/MC).
F29	CARBOHD	620	630	N-LINKED (GLC/MC).
F30	CARBOHD	630	640	N-LINKED (GLC/MC).
F31	CARBOHD	640	650	N-LINKED (GLC/MC).
F32	CARBOHD	650	660	N-LINKED (GLC/MC).
F33	CARBOHD	660	670	N-LINKED (GLC/MC).
F34	CARBOHD	670	680	N-LINKED (GLC/MC).
F35	CARBOHD	680	690	N-LINKED (GLC/MC).
F36	CARBOHD	690	700	N-LINKED (GLC/MC).
F37	CARBOHD	700	710	N-LINKED (GLC/MC).
F38	CARBOHD	710	720	N-LINKED (GLC/MC).
F39	CARBOHD	720	730	N-LINKED (GLC/MC).
F40	CARBOHD	730	740	N-LINKED (GLC/MC).
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F42	CARBOHD	750	760	N-LINKED (GLC/MC).
F43	CARBOHD	760	770	N-LINKED (GLC/MC).
F44	CARBOHD	770	780	N-LINKED (GLC/MC).
F45	CARBOHD	780	790	N-LINKED (GLC/MC).
F46	CARBOHD	790	800	N-LINKED (GLC/MC).
F47	CARBOHD	800	810	N-LINKED (GLC/MC).
F48	CARBOHD	810	820	N-LINKED (GLC/MC).
F49	CARBOHD	820	830	N-LINKED (GLC/MC).
F50	CARBOHD	830	840	N-LINKED (GLC/MC).
F51	CARBOHD	840	850	N-LINKED (GLC/MC).
F52	CARBOHD	850	860	N-LINKED (GLC/MC).
F53	CARBOHD	860	870	N-LINKED (GLC/MC).
F54	CARBOHD	870	880	N-LINKED (GLC/MC).
F55	CARBOHD	880	890	N-LINKED (GLC/MC).
F56	CARBOHD	890	900	N-LINKED (GLC/MC).
F57	CARBOHD	900	910	N-LINKED (GLC/MC).
F58	CARBOHD	910	920	N-LINKED (GLC/MC).
F59	CARBOHD	920	930	N-LINKED (GLC/MC).
F60	CARBOHD	930	940	N-LINKED (GLC/MC).
F61	CARBOHD	940	950	N-LINKED (GLC/MC).
F62	CARBOHD	950	960	N-LINKED (GLC/MC).
F63	CARBOHD	960	970	N-LINKED (GLC/MC).
F64	CARBOHD	970	980	N-LINKED (GLC/MC).
F65	CARBOHD	980	990	N-LINKED (GLC/MC).
F66	CARBOHD	990	1000	N-LINKED (GLC/MC).
F67	CARBOHD	1000	1010	N-LINKED (GLC/MC).
F68	CARBOHD	1010	1020	N-LINKED (GLC/MC).
F69	CARBOHD	1020	1030	N-LINKED (GLC/MC).
F70	CARBOHD	1030	1040	N-LINKED (GLC/MC).
F71	CARBOHD	1040	1050	N-LINKED (GLC/MC).
F72	CARBOHD	1050	1060	N-LINKED (GLC/MC).
F73	CARBOHD	1060	1070	N-LINKED (GLC/MC).
F74	CARBOHD	1070	1080	N-LINKED (GLC/MC).
F75	CARBOHD	1080	1090	N-LINKED (GLC/MC).
F76	CARBOHD	1090	1100	N-LINKED (GLC/MC).
F77	CARBOHD	1100	1110	N-LINKED (GLC/MC).
F78	CARBOHD	1110	1120	N-LINKED (GLC/MC).
F79	CARBOHD	1120	1130	N-LINKED (GLC/MC).
F80	CARBOHD	1130	1140	N-LINKED (GLC/MC).
F81	CARBOHD	1140	1150	N-LINKED (GLC/MC).
F82	CARBOHD	1150	1160	N-LINKED (GLC/MC).
F83	CARBOHD	1160	1170	N-LINKED (GLC/MC).
F84	CARBOHD	1170	1180	N-LINKED (GLC/MC).
F85	CARBOHD	1180	119	

Query Match	05.16	
Best Local Similarity	83.3%	
Conservative	0	
Mismatches	1	
Indels	0	
Gaps	0	

QY	1	PTOPQG	6
Db	213	PTOPSG	218

```

      RESULT      8
      PR06_YEAST
      ID          PR06 YEAST
      STANDARD:
      PRT:      899 AA.

```

[illegible]

RN [2]
 RP SEQUENCE FROM H.A.
 RC STRAIN-S280C
 RX MEDLINE: 9531020
 RA ALIHOVIC A., POLJ T. M.:
 R7 "Sequence and analysis of 24 kb on chromosome 11 of Saccharomyces
 R8 cerevisiae." *Yeast* 7:479-493,1995.
 RL TEST SUBJECTS INVOLVED IN PRE-MRNA SPLICING.

CC - SPECIFICITY LOCATION: NUCLEAR.
CC
CC - SIMILARITY TO SOME OTHER PRE-MRNA SPLICING FACTORS.
CC
CC - SIMILARITY CONTAINS 10 PER DOMAINS.
CC
CC
CC This swiss-prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC

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CC or send an email to license@isb-sib.ch).

[illegible]

```

RESULT      9
CNG4_BOVIN
ID          CNG4_BOVIN
AC         0281B1: 028082:

```

DT 0-MAY-2000 (Rel. 39, Last annotation update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 240 KDA PROTEIN OF ROD PHOTORECEPTOR CMG-CH
DE 240 KDA PROTEIN OF ROD PHOTORECEPTOR CMG-CH

[illegible]

RN
 RE: JOURNAL OF 454-1394 FROM N.A.
 RN
 RE: TISSUE-TESTS:
 RN
 RE: MEDLINE: 9618096.
 RN
 RE: Biel M., Zeng X., Ludwig A., Sautter A., Hofmann F.:
 RN
 RE: "Molecular cloning and expression of the modulatory subunit of the
 RN
 RE: cyclic nucleotide-gated cation channel".
 RN
 RE: J. Biol. Chem. 271:6349-6355(1996).
 RN
 RE: [3]

RP SEQUENCE OF 1-590 FROM N.A.
RC TISSUE-RETININ;
RC Sugimoto Y., Yatsunami K., Tsujimoto M., Kozono H.G., Ichikawa A.;
RL Substituted (XX-191) to the EMBL/Cambium/CDU databases.
CC -1- SUBUNIT; FORMS FUNCTIONAL HETEROLIGOMERIC CHANNELS WITH CMG3.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

Page 5

[illegible][illegible]

us-09-308-237b-1.rsp

Search completed: November 16, 2000, 15:38:22
Job time: 108 sec

```

Query Match:      82.94;  Score 29;  DB 1;  Length 162;
Best local similarity: 83.34;
Prod. NO. 41;
Matches 5;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0.
QY      1  PROPG 6
        1 1111
DB      346  PROPG 151

```

RESULT 19

STANDARD; PRT; 175 AA.

01-MAY-1992 (ROL, 22, Created)
01-MAY-1992 (ROL, 22, Created)

30-MAY-2000 (Rel. 39, large annotation update)

SSB. (HELIX-DESTABILIZING PROTEIN)

Sorbatia marcescens

OC Serratia, gamma subdivision; Enterobacteriaceae;

SEQUENCE FROM N 2

STRAINS 1;

do Vries J., Wacke

...rolling and sequencing of
single-stranded DNA-biotin...

Gene 127:39-45 (1993).

CHARACTERIZATION.

de Vries J. A. Genschel T

The single-stranded-DNA-binding

Kur. J. Biochem. 224:613-622

CONCLUSION: THIS PROTEIN IS
CHROMOSOMES AND ITS STING

INVOLVED IN DNA RECOMBIN

-1- SIMILARITY: BELONGS TO T

This SWISS-PROT entry is con-

between the Swiss Institute
the European Parliament

use by non-profit institutions

and this statement is

or send an email to licensing@wiley.com

EMBL: X65080; CAA46208.1; -

ISSN: P02339-1K&M

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INTERPRD; IPR000424; -
PRAM; PR00425; -
```

PROS14E; PS00735; \$5B_1\$; 1.

DNA-binding: DNA -seq: 1.

```
INIT_MET 0
DNA_BIND 0
```

SEQUENCE 175 AA; 18678 MW;

Query Match: 82.9%

Matches	5; Conservative	0; Non-conservative
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2	1	0
3	1	0
4	1	0
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92	1	0
93	1	0
94	1	0
95	1	0
96	1	0
97	1	0
98	1	0
99	1	0
100	1	0

1. PROPOS 6

125 11111

1

Genome version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using nr model

Run on: November 16, 2000, 15:36:10 | Search time 18.12 seconds
30.919 Million coll updates/sec

US-09-308-237b-1

Perfect score: 15

Sequence: 1 PTC006 6

Scoring table: BLAST/MSD

gapop: 10.0, gapext: 0.5

Searched: 237973 seqs, 9371336 residues

Total number of hits satisfying chosen parameters: 237973

Minimum db seq length: 0

Maximum db seq length: 2600000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Matching filter to summarize

Database: 1: SPT398L_14.1
2: SPT398L_14.1
3: SPT398L_14.1
4: SPT398L_14.1
5: SPT398L_14.1
6: SPT398L_14.1
7: SPT398L_14.1
8: SPT398L_14.1
9: SPT398L_14.1
10: SPT398L_14.1
11: SPT398L_14.1
12: SPT398L_14.1
13: SPT398L_14.1
14: SPT398L_14.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the observed score.
score greater than or equal to the observed score.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	35	100.0	573	4	016671
2	32	91.4	702	2	029024
3	32	91.4	702	2	029024
4	32	91.4	702	2	029024
5	31	88.6	700	13	029188
6	31	88.6	700	13	029188
7	31	88.6	700	13	029188
8	31	88.6	700	13	029188
9	31	88.6	700	13	029188
10	31	88.6	700	13	029188
11	31	88.6	700	13	029188
12	31	88.6	700	13	029188
13	31	88.6	700	13	029188
14	31	88.6	700	13	029188
15	31	88.6	700	13	029188
16	31	88.6	700	13	029188
17	31	88.6	700	13	029188
18	31	88.6	700	13	029188
19	31	88.6	700	13	029188

20	30	85.7	702	10	029024
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23	30	85.7	702	10	029024
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25	30	85.7	702	10	029024
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27	30	85.7	702	10	029024
28	30	85.7	702	10	029024
29	30	85.7	702	10	029024
30	30	85.7	702	10	029024
31	30	85.7	702	10	029024
32	30	85.7	702	10	029024
33	30	85.7	702	10	029024
34	30	85.7	702	10	029024
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36	30	85.7	702	10	029024
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38	30	85.7	702	10	029024
39	30	85.7	702	10	029024
40	30	85.7	702	10	029024
41	30	85.7	702	10	029024
42	30	85.7	702	10	029024
43	30	85.7	702	10	029024
44	30	85.7	702	10	029024
45	30	85.7	702	10	029024

ALIGNMENTS

RESULT 1

U	016671	PRELIMINARY	PR: 573 NA.
AC	016671	01702	
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[illegible]

Query Match	85.7%	Score 30	DB 1.3	Length 297
Best Local Similarity	83.3%	Prod. No. 95		
Matches	5	Conservative	0	Mismatches
			1	Indels
			0	Gaps
			0	
Qy	1	PROPOS	6	
		1	1	1
		1	1	1
Db	158	PROPOS	163	

[illegible]

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Query Match      85.7%   Score 30:  DB 2:   Length 296:
Host Local Similarity  83.3%   Prod. No. 95:
Matches      5:  Conservative  0:  Mismatches      1:  Indels      0:  Gaps      0:

QY      1  ProDoc 6
        | | | | |
Db      125 PaProC 130

```

Search completed: November 16, 2000, 15:38:10
Job time: 120 sec

OY 1 PROPOS 6
 DB 137 Pctgns 142
 R50927 6
 ID R53642 standard: Protein, 374 AA.
 XX M3642.
 XX 13-JUN-1997 (first entry)
 DE Human alpha(1,3)-fucosyltransferase (Fuc-TV).
 KM Alpha(1,3)-fucosyltransferase; Lewis enzyme; Fuc-TV.
 KM 9-glycosylidase; oligosaccharidase; blood group.
 XX OS Homo sapiens.
 FH Key
 F7 Domain
 F7 16-34
 F7 /label: Transmembrane_domain
 F7 /label: Catalytic_domain
 XX M0570421-A1.
 XX 13-MAR-1997.
 PE 06-SEP-1995: 96MD-0513816.
 XX 08-SEP-1995: 9505-0525008.
 XX (UNMT) UNIV MICHIGAN.
 PA Loggait DJ. Love JH.
 P1 WPI: 1397-35289/17.
 DR M-7680: 781679.
 XX New recombinant fucosyltransferase proteins - useful for modifying
 PT cell surface oligosaccharide structures.
 PS Example 5: Page 288-289, 329pp; English.
 CC Human GRP-Fuc-beta-D-Glc(1,4)-D-GlcNAc6 alpha(1,3)-fucosyltransferase
 CC (Fuc-TV) (M3642) can utilize neutral type 1 oligosaccharides.
 CC precursor but cannot efficiently utilize type 1 oligosaccharides.
 CC obtained from a human gene that was cloned from an isolated DNA sequence.
 CC T61675) as probe. The Fuc-TV cDNA, when expressed de novo
 CC expression of functions within mammalian cells to generate de novo
 CC are recognized by antibodies against SSEA-1, Lewis x or sialyl.
 CC Lewis x.
 SO Sequence 374 AA.
 Query Match 88.6% Score 31; DB 19;
 Best Local Similarity 83.3%; Pred. No. 26/02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 PROPOS 6
 DB 137 Pctgns 142
 R50927 7
 ID R50992
 ID Y06992 standard: Protein, 20 AA.
 XX Y06992.
 XX 22-JUL-1999 (first entry)
 DE Human glial fibrillary acidic protein GRAP mutant fragment 1.
 KM Human beta-amyloid precursor protein, beta-APP; diagnosis: cancer;
 KM frameshift mutation; age-related disease; neurodegenerative;
 KM Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal
 KM butchery disease; neurodegenerative; neurodegenerative;
 KM diabetes mellitus type II; Alzheimer's disease; Alzheimer's
 KM ubiquitin B; apolipoprotein E; MNP2; neurofilament-L; neurofilament-M;
 KM glial fibrillary acidic protein; p53; p53; p53; p53; p53; p53;
 KM hcl-2; B-cell; leukemia/lymphoma 2 proto-oncogene; MNP-C; MNP-1;
 KM high mobility group protein-C; neuroendocrine specific protein A.
 XX OS Synthetic.
 FH Homo sapiens.
 F7 M05845322-A2.
 F7 15-OCT-1998.
 FR 02-APR-1998: 98MD-1800705.
 FR 10-APR-1997: 9705-0043153.
 XX (UNMT) RIKENGENE PROJECT
 PA (RGA) RIKENGENE PROJECT
 PA (Y0692) UNIV NOTREDAME ELASMUS
 PA Butch JH, Grosfeld PG, Van Leeuwen JW.
 DR M-7680: 473784.
 XX Diagnosing disease by detecting frameshift mutations in RNA or
 PT neurological diseases - used to diagnose cancer and
 PT neurological diseases - used to diagnose cancer and
 PT for treatment and prevention with specific ribozymes or wild-type
 XX RNA.
 PS Disclosure: Figure 13: 258pp; English.
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, a frameshift mutation in a nucleic acid
 CC mutation. The method is used to diagnose age-related disease (e.g., Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, neuronal butchery
 CC multiple sclerosis), alcoholic liver disease, Huntington's disease, IT
 CC and many others listed) or susceptibility to these disorders. The method
 CC at an early stage. It is based on Alzheimer's disease in living patients.
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC beta-amyloid precursor protein, specifically proteins including
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, neurofilament-L,
 CC neurofilament-M, p53, p53, p53, p53, p53, p53, p53, p53, p53, p53,
 CC protein (GRAP), the cellular tumour antigen p53, the cellular tumour antigen
 CC 2 (hcl-2) proto-oncogene, semaphorin III, MNP-1, high mobility group
 CC protein-C (MNP-C) and neuroendocrine specific protein A.
 SO Sequence 20 AA.
 Query Match 85.7% Score 30; DB 19;
 Best Local Similarity 81.3%; Pred. No. 16;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 PROPOS 6

OY 1 PROT00C 6
 AC 11-111111
 DB 20 P1009 25
 R1009 10
 P50761
 P50761 standard: Protoclin; 74 AA.
 AC P50761;
 DB 08-NOV-1991 (first entry)
 DE Antigenic protein encoded by clone Jambda95.1(8).
 KW Material: vaccine; antigen; epitope.
 XX Plasmidium falciparum K1 isolate (Thailand).
 XX Key
 FH Location/Qualities
 FT 32-49 epitope 5.1-1
 FT /note: repeat: see comments*
 FT Peptide
 XX WP513189-A.
 XX
 PD 28-NOV-1985: 85EF-0031110.
 PF 19-FEB-1985:
 XX 21-DEC-1984: 84GH-0031317.
 XX 21-DEC-1984: 84GH-0031317.
 PR 13-NOV-1984: 84CH-0028643.
 XX
 XX (NMR) NATIONAL RES RES CORP.
 PI Hopo 1A, Saito JB, Strachbachova-Medvide J;
 DR NPI: 1985-211745/35.
 DR N-PS08; N00531.
 XX Antigenic material for vaccination against malaria
 PT Amino acid residues sequence of natural antigen and
 PT intra-erythrocytic forms of plasmidium parasites.
 PS
 PS Disclousure: Fig 2a: 70pp: English.
 XX
 XX The sequence was deduced from a DNA insert from clone
 CC and used for the synthesis of an intra-erythrocytic
 CC stages of the parasite. The antigen is present as a sporozoite
 CC surface epitope. The 5.1-1 epitope comprises a sequence homologous
 CC to the 5.1-1 epitope of the parasite. The 5.1-1 epitope
 CC protein (NMR). The 5.1-1 epitope appears to be made of
 CC sequences of seven and eight residues respectively linked by three
 CC may be omitted from antigenic material do not contribute to antigenicity and
 CC express antigenic peptides useful for the prep. of vaccines for
 CC protection against malaria. See also P51201.
 XX
 XX Sequence 74 AA:
 Query Match 82.94% Score 29; DB 6; Length 74;
 Best Local Similarity 83.34% Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 PROT00C 6
 DB 58 P1009 63
 R1009 11
 Y21354
 Y21354
 ID Y21354 standard: Protein; 125 AA.
 AC Y21354;
 DB 22-NOV-1999 (first entry)
 XX
 XX Human HSP-70 mutant protein fragment 6.
 DE
 XX (human) beta-amyloid precursor protein; beta-amyloid; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegeneration;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW ubiquitin B; apolipoprotein B; A2; neurofilament-C; neurofilament; tau;
 KW neurofilament; tau; presenilin II; presenilin II; cellular tumor antigen;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; BCR-C; NSP4-1;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX
 OS Synthetic.
 OS Homo sapiens.
 RM K09645322-42.
 PD 15-OCT-1998.
 PF 02-APR-1998: 98MC-1B00705.
 XX 10-APR-1997: 97US-0043161.
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 XX (OYR-) R1350N1Y UTRCIC.
 PA (RCN-) ROYAL NETHERLANDS ACID NUTS S. SCI.
 XX (YRNC) NUTR NUTRITION NUTRITION.
 XX
 PI Buttnach JPH, Grosfeld FG, van Loenen FW;
 DR NPI: 1998-609901/51.
 DR N-PS08; X73768.
 XX
 XX Disclousure: Figure 17; 25pp: English.
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method involves the use of a probe that is complementary
 CC to the RNA molecule and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease, II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC caused by mutations in RNA rather than DNA. The method also allows
 CC use of neuronal system RNA molecules, specifically proteins including
 CC protein-amyloid precursor protein (beta-APP), the microtubule associated
 CC associated protein 3 (MAP3), neurofilament-L, neurofilament-W,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), tau, and the amyloid precursor protein (APP). The method
 CC protein-C (bcl-2) and neuroendocrine specific protein A.
 XX
 XX Sequence 125 AA:
 Query Match 82.94% Score 28; DB 19; Length 125;
 Best Local Similarity 83.34% Pred. No. 15+42;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

0Y 1 PROPG 6
14 11111
14 pepqys 19

RESULT 12

ID 173845 standard: Protein: 127 AA.

73845

AC 173845:

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XX herbicide; antiparasitic agent; ruminant growth promoter;
XX bioreductase; receptor agonist; antiparasitic; biomass.
XX Streptomyces griseus.
XX WC020000613-AL.

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XX 28-AUG-1985.
XX 19-FEB-1985: 85BP-010110.
XX 21-FEB-1984: 84CB-002327.
XX 21-FEB-1984: 84CB-002327.
XX 13-MAY-1984: 84CB-002863.
XX (MNR) WNTONM, RES DEV COMP.
P1 Hope J.A., Seale J.G., Streptococcus-McArdle J.
WPI 1985-111742/75.
XX This sequence was deduced from a DNA insert from clone lambda92.1(9)
XX which encodes a protein that is the major surface antigen of the
XX parasite. The antigen is present as a sporozoite surface epitope.
XX The 5.1-1 epitope comprises a sequence homologous with the tandemly
XX repeated region of the parasite. The 5.1-1 epitope appears to be made up of two sequences of seven
XX and eight residues respectively. Linked by three residues, Ser-Glu-
XX from synthetic antigens. The DNA can be used to express antigenic
XX peptides useful for the prepn. of vaccines for protection against
XX malaria. See also P0761.
XX Sequence 162 AA.
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Genome version 4.5
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ON proteins - protein search, using SW model

Run on: November 8, 2000, 14:55:13 | Search time 12.24 seconds
8,216 Million cell updates/sec
without alignments

Title: US-09-308-237B-1

Accession score: 1 FTD003 6

Sequence: 1 FTD003 6

Scoring table: HUSONM62

Gapop 10.0, Gapcut 0.5

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Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing files 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than the observed score, result being printed.

score greater than the observed score, result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

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3	31	88.6	374	1	US-08-696-721-11	Sequence 11, Appl
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5	29	82.3	165	2	US-08-319-704-6	Sequence 3, Appl
6	29	82.3	165	2	US-08-319-704-6	Sequence 3, Appl
7	29	82.3	459	3	US-09-118-319-6	Sequence 7, Appl
8	29	82.3	483	2	US-08-749-301-2	Sequence 2, Appl
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10	29	82.3	755	3	US-09-071-101-2	Sequence 2, Appl
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Patent No. 111458
GENERAL INFORMATION:
APPLICANT: Li, Xin-Liang
APPLICANT: Chen, Huizhong
APPLICANT: Ljungdahl, Lars G.
TITLE OF INVENTION: Ophiomyces Cellulase Celf Protein and Coding Sequences
FILE REFERENCE: 33-98sequence listing
CURRENT APPLICATION NUMBER: US/09/118,319

Thu Nov 16 15:44:25 2000

us-09-308-237b-1_1.rai

Page 4

: CURRENT FILING DATE: 1998-07-17
 : NUMBER OF SEQ ID NOS: 9
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 6
 : LENGTH: 459
 : TYPE: prt
 : ORGANISM: Orf1omyces sp. pc-2
 US-09-118-319-6

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05-08-74-49-391-2
Sequence 2, Application US/08/45391
Patent No. 5948657
INVENTOR:
APPLICANT: Chem9, Kyo-to-kan
APPLICANT: Sallinger, Leonard B.
APPLICANT: Liu, Jia-hao
APPLICANT: Erdosy, Cecil M.
APPLICANT: Moloney, Maurice M.
TITLE OF INVENTION: A system obtained from an
NUMBER OF SEQUENCES: 6
CORRESPONDENT ADDRESS: Warner and Sullivan, P.C.
STREET: 5310 Washington Circle, Suite 201
CITY: Boulder
STATE: Colorado
ZIP: 80803
COMPITER READABLE FORM:
MODERN TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/74-391
FILING DATE: 13-Nov-1995
CLASSIFICATION: 415
NAME: DORIN M. PETERSON
REGISTRATION NUMBER: 31,878
REFERENCE/DOC# NUMBER: 93-95
TELEPHONE: (303) 439-8000
TELEFAX: (303) 439-8000
INVENTOR: DORIN M. PETERSON
ADDRESS: 1400 CHERRY STREET, 100
CITY: BOULDER, CO 80501
LENGTH: 485 amino acids
TYPE: amino acid
MOLECULE TYPE: protein

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Db 331 PPOPG 336

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RESULT 9
US-86-0156-104.2
Patent No. 5555270
GENERAL INFORMATION
INVENTOR: Alan
TITILE OF INVENTION: EXPLOITATION OF THE CELLULOSE COMPLEX
APPLICANT: Palish, John R.
NUMBER OF SOURCES: 1
CORRESPONDENCE ADDRESS: Jackson, RM
STREET: Floor
CITY: Newkirk
STATE: Maryland
COUNTRY: USA

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db 474 PROPOS 479

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US980774101
 1 Application US/98071101
 2 Patent No. 4013503
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 4 GENERAL INFORMATION:
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 6 APPLICANT: Lok, SI
 7 APPLICANT: Jacques, Stephen R.
 8 APPLICANT: RYAN PHARMORONE CONVERTASE
 9
 10 NUMBER OF SEQUENCES:
 11
 12 CORRESPONDING ADDRESS:
 13
 14 ADDRESSEE: ZymoGenetics, Inc.
 15 STREET: 1201 Eastlake Avenue East
 16 CITY: Seattle
 17 STATE: WA
 18 COUNTRY: USA
 19 ZIP: 98102

Thu Nov 16 15:44:25 2000

us-09-308-237b-1.1.ra1

Page 7

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or 1 PPOPG 6
11111
DB 407 PPOPG 412

Search completed: November 8, 2000, 14:37:57
Job time: 164 sec

The first part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The second part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The third part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The fourth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The fifth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The sixth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The seventh part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The eighth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The ninth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The tenth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

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OK protein - protein search using sw model

Run on: November 8, 2000, 14:37:18 : Search time 36.88 Seconds

Title: US-09-308-237b-1

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Sequence: 1570096 6

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Total number of hits satisfying chosen parameters: 863609

Maximum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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38	30	85.7	110	21	US-60-144-508-3365	Sequence 3365, Ap
39	30	85.7	110	21	US-60-144-508-3365	Sequence 3365, Ap
40	30	85.7	110	21	US-60-144-508-3365	Sequence 3365, Ap
41	30	85.7	110	21	US-60-144-508-3365	Sequence 3365, Ap
42	30	85.7	110	21	US-60-144-508-3365	Sequence 3365, Ap
43	30	85.7	110	21	US-60-144-508-3365	Sequence 3365, Ap
44	30	85.7	110	21	US-60-144-508-3365	Sequence 3365, Ap
45	30	85.7	110	21	US-60-144-508-3365	Sequence 3365, Ap

ALIGNMENTS

RESULT: 1
Sequence 1, Application US/0908237B
GENERAL INFORMATION:
APPLICANT: TOMISHERA, MSAKI
APPLICANT: YAMADA, ARIKA
APPLICANT: INZAKAWA, TOSIYUKI
FILE REFERENCE: 0018-1052-08CT
CURRENT APPLICATION NUMBER: US/99/09/308, 237B
PRIOR APPLICATION NUMBER: PCT/JP97/04193
PRIOR FILING DATE: 1997-11-18
PRIOR FILING DATE: 1995-11-25
NUMBER OF SEQ ID NOS: 1
SEQ ID NO 1
LENGTH: 6
FEATURE: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence:peptide
LOCATION: (1) US
OTHER INFORMATION: 4-hydroxy
LOCATION: (2)

OTHER INFORMATION: hydroxy, substituted phenyl
 LOCATION: (3) RES
 OTHER INFORMATION: hydroxy substituted
 LOCATION: (4) RES
 OTHER INFORMATION: 3-hydroxy, 4-methyl proline
 NAME/REF: MOD.RES
 OTHER INFORMATION: hydroxy substituted
 NAME/REF: MOD.RES
 OTHER INFORMATION: hydroxy ethyl substituted
 OTHER INFORMATION: glycine at position 6 is linked to Proline at
 US-09-308-237b-1

Query Match 100.0% Score 35, DB 25, Length 6;
 Best Local Similarity 100.0%; Pred. No. 7, Seq=05
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PROTOP 6
 DB 1 PROTOP 6

RESULT 2
 Sequence 13, Application PC/T08941643
 GENERAL INFORMATION: INC.
 APPLICANT: CATE, Richard L.
 TITLE OF INVENTION: POLYPEPTIDES AND ANTIPODES THEREOF
 CURRENT APPLICATION NUMBER: US/08/173,412
 FILING DATE: 23-DEC-1993
 ADDRESS: C/O FISH & BEAVE
 STREET: 1221 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: COMPAQ DOS
 SOFTWARE: Patentia Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 23-DEC-1993
 CLASSIFICATION:
 PRIORITY:
 APPLICATION NUMBER: US 08/166,333
 FILING DATE: 13-DEC-1993
 APPLICATION NUMBER: US 08/173,412
 FILING DATE: 23-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 27,734
 REFERENCE/OTHER NUMBER: B7ACIP
 TELEPHONE: (212) 596-9090
 TELEFAX: (212) 596-9000
 INVENTOR: SRODNIK, CHASID N. DO NOT
 TYPE: 573 amino acids
 LENGTH: 573
 MOLECULE TYPE: Peptide

FEATURE:
 NAME/REF: Drosila
 LOCATION: 11-144
 OTHER INFORMATION: /note- "extracellular domain"
 FEATURE:
 NAME/REF: Drosila
 LOCATION: 11-130
 OTHER INFORMATION: /note- "transmembrane region"
 FEATURE: Drosila
 LOCATION: 171-573
 OTHER INFORMATION: /note- "cytoplasmic domain"
 PC/T0894-1643-13

Query Match 100.0% Score 35, DB 1, Length 573;
 Best Local Similarity 100.0%; Pred. No. 3, Seq=03
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PROTOP 6
 DB 369 PROTOP 374

RESULT 3
 Sequence 21543, Application US/00191637
 GENERAL INFORMATION:
 APPLICANT: Ventec, J. Craig
 TITLE OF INVENTION: ACID OPERATION WITH COMPENSATION
 CURRENT APPLICATION NUMBER: US/00/191,637
 FILING DATE: 2000-03-23
 ADDRESS: FISH & BEAVE
 STREET: 1221 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: COMPAQ DOS
 SOFTWARE: Patentia Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 23-DEC-1993
 CLASSIFICATION:
 PRIORITY:
 APPLICATION NUMBER: US 08/166,333
 FILING DATE: 13-DEC-1993
 APPLICATION NUMBER: US 08/173,412
 FILING DATE: 23-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 27,734
 REFERENCE/OTHER NUMBER: B7ACIP
 TELEPHONE: (212) 596-9090
 TELEFAX: (212) 596-9000
 INVENTOR: SRODNIK, CHASID N. DO NOT
 TYPE: 573 amino acids
 LENGTH: 573
 MOLECULE TYPE: Peptide

Query Match 91.4% Score 32, DB 21, Length 601;
 Best Local Similarity 83.3%; Pred. No. 1, Seq=03
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PROTOP 6
 DB 338 PROTOP 343

RESULT 4
 Sequence 6013, Application US/00191681
 GENERAL INFORMATION:
 APPLICANT: LI, Peter, M. D.
 TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
 ACID SEQUENCES AND METHODS FOR IDENTIFYING ISOLATED DROSOPHILA PROTEINS AND
 NUCLEIC ACID SEQUENCES
 CURRENT APPLICATION NUMBER: US/00/191,681
 FILING DATE: 2000-03-23
 ADDRESS: FISH & BEAVE
 STREET: 1221 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: COMPAQ DOS
 SOFTWARE: Patentia Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 23-DEC-1993
 CLASSIFICATION:
 PRIORITY:
 APPLICATION NUMBER: US 08/166,333
 FILING DATE: 13-DEC-1993
 APPLICATION NUMBER: US 08/173,412
 FILING DATE: 23-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 27,734
 REFERENCE/OTHER NUMBER: B7ACIP
 TELEPHONE: (212) 596-9090
 TELEFAX: (212) 596-9000
 INVENTOR: SRODNIK, CHASID N. DO NOT
 TYPE: 573 amino acids
 LENGTH: 601
 MOLECULE TYPE: Peptide

Query Match: 91.4%; Score 32; DB 21; Length 601;
 Best Local Similarity: 83.3%; Pred. No. 8e+02;
 Matches: 5; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;
 Oy: 1 PROPOS 6
 DB: 338 PIRGOS 343

RESULT 5
 PCT-US99-22317-1
 Sequence 1, Application: PCT/US9532517
 APPLICANT: THE TRUSTEES OF COLUMBIA UNIVERSITY, IN THE CITY OF
 TITLE OF INVENTION: Gene Encoding pVLA
 CURRENT APPLICATION NUMBER: PCT/US99/25517
 CURRENT FILING DATE: 1995-09-29/09/162,524
 EXAMINER FILING DATE: 1998-09-29
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 1
 LENS: 300
 TYPE: PCT
 PCT-US99-22317-1
 Query Match: 88.6%; Score 31; DB 11; Length 300;
 Best Local Similarity: 83.3%; Pred. No. 8e+02;
 Matches: 5; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;
 Oy: 1 PROPOS 6
 DB: 238 PIRGOS 243

RESULT 6
 US-09-162-524-1
 Sequence 1, Application US/0916554
 APPLICANT: JESSALI, Thomas M.
 TITLE OF INVENTION: Gene encoding MMR2 and uses thereof
 TITLE REFERENCE: 51477/pvLA/US/09/162,524
 CURRENT FILING DATE: 1998-09-25
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 1
 LENS: 300
 TYPE: PCT
 US-09-162-524-1
 Query Match: 88.6%; Score 31; DB 16; Length 300;
 Best Local Similarity: 83.3%; Pred. No. 8e+02;
 Matches: 5; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;
 Oy: 1 PROPOS 6
 DB: 238 PIRGOS 243

RESULT 7
 US-09-443-704-12
 Sequence 12, Application US/09443704
 APPLICANT: CAHOON, Rebecca E.
 APPLICANT: LNU, Shan-310

APPLICANT: ODELL, Joan
 APPLICANT: BARTALSKI, Antoni
 APPLICANT: MMS, Jude
 TITLE OF INVENTION: Plant MMR-related transcription factors
 TITLE REFERENCE: PCT/US99/25517
 CURRENT APPLICATION NUMBER: US/09/443,704
 CURRENT FILING DATE: 1999-11-19
 EXAMINER APPLICATION NUMBER: 6109,294
 EXAMINER FILING DATE: 2000-02-07/1598
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: Microsoft Office 97
 SEQ ID NO: 1
 LENS: 302
 TYPE: PCT
 US-09-443-704-12
 Query Match: 88.6%; Score 31; DB 18; Length 302;
 Best Local Similarity: 83.3%; Pred. No. 8e+02;
 Matches: 5; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;
 Oy: 1 PROPOS 6
 DB: 220 PIRGOS 225

RESULT 8
 US-09-231-489-11
 Sequence 11, Application US/0823489
 APPLICANT: MCGILL, JOHN B.
 TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS OF POLYNUCLEOTIDES OR AS FREE MOLECULES, AND FOR THE ISOLATION OF POLYNUCLEOTIDES OR AS FREE MOLECULES THAT DETERMINE THESE STRUCTURE
 NUMBER OF SEQUENCES: 14
 ADDRESSER: OHLON, SHYAM, MCGILLAND, MAYER & NEUSTADT, P.C.
 STREET: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: PatentIn Release 11.0, Version 11.25
 CURRENT FILING DATE: US/08/231,489
 FILING DATE: 25-MAR-1997
 APPLICATION NUMBER: 07/914,281
 PCT/US97/05671
 FILING DATE: INFORMATION:
 NAME: Javaliaye Jean-Paul M. P.
 REGISTRATION NUMBER: 31,423,060-55
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)521,4300
 TELEFAX: 248653 ORT UR
 INFORMATION FOR SEQ ID NO: 11:
 SOURCE: 374 amino acids
 TYPE: amino acid
 FUNCTION: unknown
 MOLECULAR WEIGHT: 41,815
 US-08-231-489-11

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Page 4

Query Match
Best Local Similarity: 88.64; Score 31; DB 13; Length 374;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 137 PPROG 6
11111111

RESULT 9
Sequence 11:11
US-09-042-531-11
GENERAL INFORMATION: US/09/042531
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: POLYMERIZATION OF OLIGONUCLEOTIDES TO FORM POLYMERIZATION
TITLE OF INVENTION: OLIGONUCLEOTIDES, OR AS FREE MOLECULES AND POLYMERIZATION
NUMBER OF SEQUENCES: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURE
CORRESPONDENCE ADDRESS:
ADDRESS: 8300N. SPYAK, MCLELAND, WAIR & NEUSTADT,
STREET: 1155 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: VA
COUNTRY: U.S.A.
ZIP: 22202
COMMENTS: QUOTE: WOM
MODIFY TYPE: FLOPPY disk
SOFTWARE: IBM PC compatible
CURRENT APPLICATION NUMBER: US/09/042531, version 11.25
CLASSIFICATION:
PRIORITY APPLICATION DATA:
FILING NUMBER: US/08/793,246
FILING DATE: 20-JUL-1992
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
NAME: LAYALL, JAMES M. P.
RIGHTS INFORMATION: 31-451
TELECOMMUNICATION NUMBER: 203-060-55
TELEPHONE: (703)521-4500
TELEX: (703)866-2347
TITLE: (11)11111111
INFORMATION FOR SEQ ID NOS:
SEQUENCE CHARACTERISTICS: 11:
TYPE: amino acid
TOPOLOGY: unknown
US-09-042-531-11: protein

Query Match
Best Local Similarity: 88.64; Score 31; DB 15; Length 374;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 137 PPROG 6
11111111

US-60-162-245-2777

Sequence 2777: Application US/60/16245
GENERAL INFORMATION: US/60/16245
APPLICANT: BONAZZI, VIGEN
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS AND USES
NUMBER OF SEQUENCES: 1
CURRENT FILING DATE: 1999-10-29
SOFTWARE: FASTSD FOR Windows version 4.0
SEQ ID NO 2777
TYPE: PRT
US-60-162-245-2777

Query Match
Best Local Similarity: 85.74; Score 30; DB 21; Length 48;
Matches 1
11111111
US-60-162-245-2777
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 41 PPROG 6
11111111

RESULT 11
Sequence 41:11
US-60-160-203-5935
GENERAL INFORMATION: US/60/160203
APPLICANT: BONAZZI, VIGEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
NUMBER OF SEQUENCES: 1
CURRENT FILING DATE: 1999-10-19
SOFTWARE: FASTSD FOR Windows version 4.0
SEQ ID NO 5935
TYPE: PRT
US-60-160-203-5935
TITLE: (11)11111111
INFORMATION FOR SEQ ID NOS:
SEQUENCE CHARACTERISTICS: 41:
TYPE: amino acid
TOPOLOGY: unknown
US-60-160-203-5935
OTHER INFORMATION: aa = Any Amino Acid
US-60-160-203-5935

Query Match
Best Local Similarity: 85.74; Score 30; DB 21; Length 56;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 33 PPROG 6
11111111

RESULT 12
Sequence 33:12
US-60-160-203-5935
GENERAL INFORMATION: US/60/160203
APPLICANT: BONAZZI, VIGEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
NUMBER OF SEQUENCES: 1
CURRENT FILING DATE: 1999-10-27
SOFTWARE: FASTSD FOR Windows version 4.0
SEQ ID NO 5935
TYPE: PRT
US-60-160-203-5935

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? SEQ ID NO 2970
 ? LENGTH: 58
 ? TYPE: PROT
 ? ORGANISM: HUMAN
 US-60-177-571-2970

Query Match 85.7%: Score 30; DB 21; Length 58;
 Best Local Similarity 85.7%: Score No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 1;

Or 1 PROPOS 6
 DB 16 PROPOS 21

RESULT 13
 US-60-177-571-2820
 ? Sequence Annotation: Application US/60177571

? GENERAL INFORMATION: VIVIAN
 ? APPLICANT: BOWAZZI, VIVIAN
 ? TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ? TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ? TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ? TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ? FILE REFERENCE: CLOU0164
 ? CURRENT APPLICATION NUMBER: US/60/177,571
 ? CURRENT FILING DATE: 2000-01-27
 ? NUMBER OF SEQ ID NOS: 5082
 ? SOFTWARE: PASSED FOR Windows Version 4.0
 ? SEQ ID NO 2820
 ? LENGTH: 71
 ? TYPE: PROT
 ? ORGANISM: HUMAN
 US-60-177-571-2820

Query Match 85.7%: Score 30; DB 21; Length 71;
 Best Local Similarity 85.7%: Score No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Or 1 PROPOS 6
 DB 34 PROPOS 39

RESULT 14
 US-60-160-203-4845
 ? Sequence Annotation: Application US/60160203

? GENERAL INFORMATION: VIVIAN
 ? APPLICANT: BOWAZZI, VIVIAN
 ? TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ? TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ? TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ? TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ? FILE REFERENCE: CLOU0164
 ? CURRENT APPLICATION NUMBER: US/60/160,203
 ? CURRENT FILING DATE: 1999-10-15
 ? NUMBER OF SEQ ID NOS: 6316
 ? SOFTWARE: PASSED FOR Windows Version 4.0
 ? SEQ ID NO 4845
 ? LENGTH: 76
 ? TYPE: PROT
 ? ORGANISM: HUMAN
 US-60-160-203-4845

Query Match 85.7%: Score 30; DB 21; Length 76;
 Best Local Similarity 85.7%: Score No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Or 1 PROPOS 6
 DB 34 PROPOS 39

RESULT 15
 US-60-160-203-4845
 ? Sequence Annotation: Application US/60160940

? GENERAL INFORMATION: VIVIAN
 ? APPLICANT: BOWAZZI, VIVIAN
 ? TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ? TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ? TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ? FILE REFERENCE: CLOU0164
 ? CURRENT APPLICATION NUMBER: US/60/160,940
 ? CURRENT FILING DATE: 1999-10-15
 ? NUMBER OF SEQ ID NOS: 5628
 ? SOFTWARE: PASSED FOR Windows Version 4.0
 ? SEQ ID NO 5628
 ? LENGTH: 76
 ? TYPE: PROT
 ? ORGANISM: HUMAN
 US-60-160-203-4845

Query Match 85.7%: Score 30; DB 21; Length 76;
 Best Local Similarity 83.3%: Score No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Or 1 PROPOS 6
 DB 34 PROPOS 39

Search completed: November 8, 2000, 14:39:13
 Job time: 115 sec

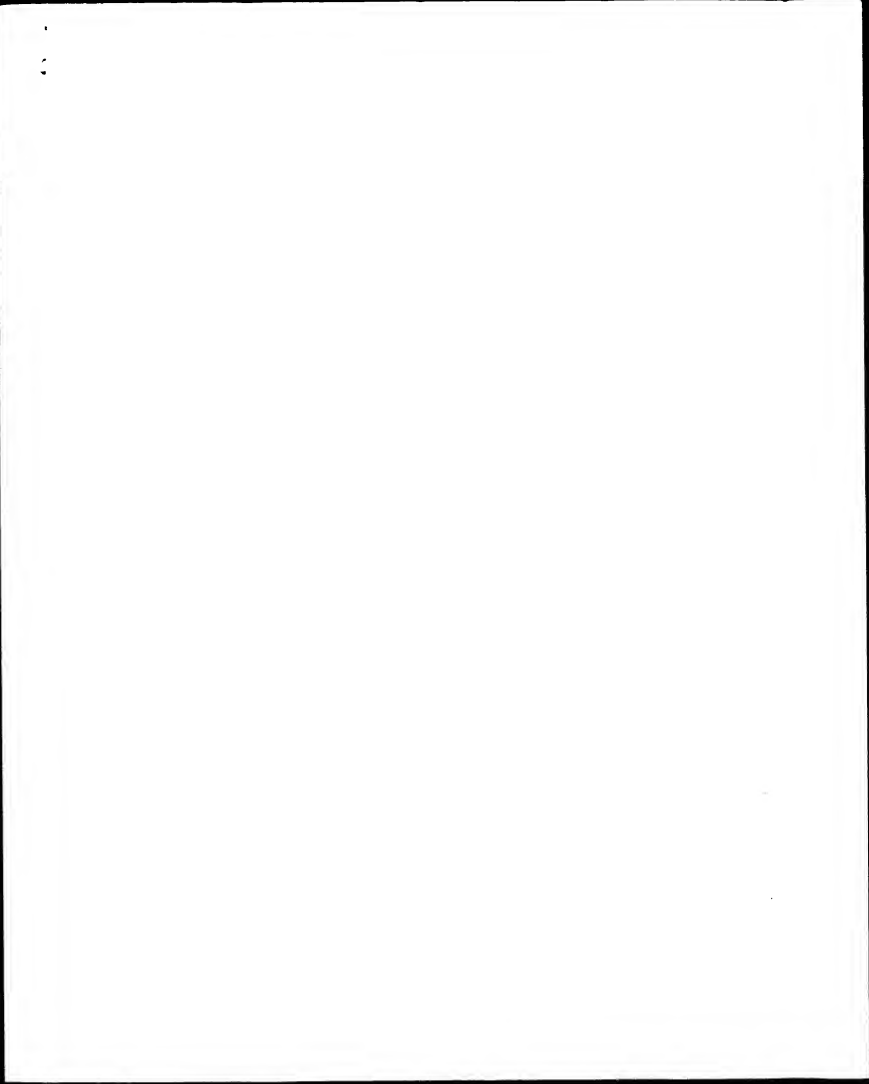
Thu Nov 16 15:44:25 2000

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A	Accession:	730990
A	Status:	Preliminary
A	Residues:	1-2262 COMA
A	Cross-references:	EMBL:AB013604; PDB:1BA3/927.1
C	Experimental source:	young tadpole larvae
C	Experimental technique:	RT-PCR
C	Accession:	TAC01
C	Specificity:	voltage-dependent calcium channel protein alpha-1 chain
C	Groupings:	calcium binding; calcium channel
D	Query Match:	
D	Score:	85.7%
D	Length:	Score 30; DB 21;
D	Mismatches:	5; Conservatively 0; Mismatches 1;
D	Indels:	0;
G	1 proposal:	6
G	1111	
G	DB	1839 Propos 1844

Search completed: November 8, 2000, 14:38:34
Job time: 200 sec



Genome version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2000, 14:38:03 | Search time 8.45 seconds

22,685 Million cell updates/sec

Title: US-09-308-237b-1

Sequence: 1 PFC006 6

Scoring table: Gap0 10.0, Gapex 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_29.*

Prod. No. is the number of results predicted by chance to have a score greater than the observed score, assuming random, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	573	1	AMH2.HUMAN
2	31	88.6	574	1	PTN2.HUMAN
3	31	88.6	574	1	PTN2.HUMAN
4	31	88.6	574	1	AMH2.HUMAN
5	30	85.7	598	1	PTN1.HUMAN
6	30	85.7	598	1	PTN1.HUMAN
7	30	85.7	573	1	CL14.HUMAN
8	30	85.7	899	1	PR06.YEAST
9	30	85.7	899	1	PR06.YEAST
10	30	85.7	2481	1	CNE4.HUMAN
11	29	82.9	4660	1	LWR2.HUMAN
12	29	82.9	4660	1	LWR2.HUMAN
13	29	82.9	40	1	HEM1.YEAST
14	29	82.9	162	1	KEL1.YEAST
15	29	82.9	175	1	SS8.YEAST
16	29	82.9	281	1	HEB2.DICOL
17	29	82.9	281	1	HEB2.DICOL
18	29	82.9	304	1	P12.YEAST
19	29	82.9	506	1	PT1.YEAST
20	29	82.9	568	1	YK1.YEAST
21	29	82.9	568	1	YK1.YEAST
22	29	82.9	719	1	YK1.YEAST
23	29	82.9	719	1	YK1.YEAST
24	29	82.9	708	1	YK1.YEAST
25	29	82.9	763	1	YK1.YEAST
26	29	82.9	1189	1	YK1.YEAST
27	29	82.9	1189	1	YK1.YEAST
28	29	82.9	1460	1	YK1.YEAST
29	29	82.9	1460	1	YK1.YEAST
30	29	82.9	2444	1	YK1.YEAST
31	29	82.9	2444	1	YK1.YEAST
32	29	82.9	2534	1	YK1.YEAST
33	29	82.9	2534	1	YK1.YEAST

34	29	82.9	2531	1	YK1.YEAST
35	29	82.9	2531	1	YK1.YEAST
36	28	80.0	144	1	RS22.HUMAN
37	28	80.0	246	1	YV2.YEAST
38	28	80.0	359	1	YV2.YEAST
39	28	80.0	359	1	YV2.YEAST
40	28	80.0	356	1	C5A.YEAST
41	28	80.0	463	1	YK1.YEAST
42	28	80.0	552	1	YK1.YEAST
43	28	80.0	552	1	YK1.YEAST
44	28	80.0	566	1	YK1.YEAST
45	28	80.0	657	1	YK1.YEAST

ALIGNMENTS

Result	ID	Accession	Standard	Ref	573 AA
1	10	AMH2.HUMAN	016671	017621	
2	31	PTN2.HUMAN	016671	017621	
3	31	PTN2.HUMAN	016671	017621	
4	31	PTN2.HUMAN	016671	017621	
5	30	PTN1.HUMAN	016671	017621	
6	30	PTN1.HUMAN	016671	017621	
7	30	CL14.HUMAN	016671	017621	
8	30	PR06.YEAST	016671	017621	
9	30	PR06.YEAST	016671	017621	
10	30	CNE4.HUMAN	016671	017621	
11	29	LWR2.HUMAN	016671	017621	
12	29	LWR2.HUMAN	016671	017621	
13	29	HEM1.YEAST	016671	017621	
14	29	KEL1.YEAST	016671	017621	
15	29	SS8.YEAST	016671	017621	
16	29	HEB2.DICOL	016671	017621	
17	29	HEB2.DICOL	016671	017621	
18	29	P12.YEAST	016671	017621	
19	29	PT1.YEAST	016671	017621	
20	29	YK1.YEAST	016671	017621	
21	29	YK1.YEAST	016671	017621	
22	29	YK1.YEAST	016671	017621	
23	29	YK1.YEAST	016671	017621	
24	29	YK1.YEAST	016671	017621	
25	29	YK1.YEAST	016671	017621	
26	29	YK1.YEAST	016671	017621	
27	29	YK1.YEAST	016671	017621	
28	29	YK1.YEAST	016671	017621	
29	29	YK1.YEAST	016671	017621	
30	29	YK1.YEAST	016671	017621	
31	29	YK1.YEAST	016671	017621	
32	29	YK1.YEAST	016671	017621	
33	29	YK1.YEAST	016671	017621	

[illegible][illegible]

Query Match 82.9% Score 29; DB 1; Length 152;

Search completed: November 8, 2000, 14:39:48

Best Local 83.3% Pred. No. 41;

Job time: 103 sec

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PROPG 6

DB 146 PROPG 151

SEQUENCE 15

SSR_SEMA STANDARD; PRT. 175 AA.

AC P2512.1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 30-MAY-2000 (Rel. 31, Last annotation update)

OR 30-MAY-2000 (Rel. 31, Last annotation update)

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OR 30-MAY-2000 (Rel. 31, Last annotation update)

us-09-308-237b-1_1.rspt

RT "HSP70 homolog functions in cell-to-cell movement of a plant virus.",
RL Proc. Natl. Acad. Sci. U.S.A. 96:14771-14776(1999).
PN (2)

RC SIKAIN=BYV-4;
BA Perevnoy V V

submitted (Sep-1999) to the EMBL/GenBank/DBJ databases

```
DR INTERPRO: IPRO01788; -;
```

DR PFAM; PF00978; RNA_dep_RNAPol2; 1.

DR PFAM: PF01660; Vmethyltransf; 1.

Query Match	88.6%	Score 31;	DB 12;	Length 3
Best Local Similarity	87.3%	Score 30;	DB 12;	Length 3

matchings: conservative: 1; mismatches: 0; indels:

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RESULT 13

ID	080529	PRELIMINARY;	PRT;	213 AA.
AC	000520			

```
DT 01-NOV-1998 (TREMBLER). 08, Created)
DT 01-NOV-1998 (TREMBLER). 08, First associated update)
```

01-JUN-2008 (ITEM#161: 14, Last annotation update)
DE F1479.12 PROTEIN.

05 *Arabidopsis thaliana* (Mouse-ear cress).

○ Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Br

$$\mathbb{R}^n \quad (1)$$

RC STRAIN=CV, COLUMBIA;
modulus of elasticity = 29,000,000

KIM
AND M., ARAUJO R., BUEHLER E., DEWAT K., FENG J., KIM C.,
OSI O., GABORNE P. I., CHIN D., SUE H., REZAKHANLOV M.

Submitted (AUG-1998) to the EMBL/GenBank/DBT databases

SQ SEQUENCE 213 AA; 22308 MW; 4216943C2CD3FB8F CRC64;

Best Local Similarity 83.3%; Pred. No. 68;

1. **Introduction**

Dh 107 P70P5G 112

013015

AC 013015;

DT 01-JUL-1997 (TREMBlere, 04, last sequence update)

DE Y BOX PROTEIN 2.

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Osteichthyes; Actinopterygii; Teleostei; Fidelestei; Ostichthyes

[illegible]

PC SEQUENCE FROM N.A.
 NC Nucleotide: 28655714.
 NA Kelsen Y., Yamashita M., Megahama Y.,
 "Isolation and characterization of goldfish γ box protein, a serum
 protein with a high molecular weight and a high pI."
 RL Eur. J. Biochem. 249:854-861(1997).
 CC -1- SIMILARITY: BELONGS TO THE GOLD-SHOCK DOMAIN (GSD) FAMILY.
 DB HSBP: P20813.LINC
 DB INTERPRO: IPR02053.
 DB PFM: PF00233 GSD
 DB HHSR: PF00233 GSD
 DB PROSITE: P560352; GOLD-SHOCK.
 NM Transcription regulation, DNA-binding
 SO SEQUENCE: 297 AA; 31773 MW; 506049568876793 Cnct4.

Query Match
 Query Local Similarity 85.7% Score 30; DB 13; Length 297;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 PROPOC 6
 DB 158 PROPOC 163

RESULT 15
 ORFV01-2000 PRELIMINARY: PRT: 298 AA.
 AC ORFV70:
 TR 01-MAY-2000 (TRIMM:rel. 13, Created)
 TR 01-MAY-2000 (TRIMM:rel. 13, Deleted)
 TR 01-JUN-2000 (TRIMM:rel. 14, Last annotation update)
 NE UNICAS:
 OS Delinococcus radiodurans
 OC Bacteria; Thermus/Delinococcus group; Delinococcales; Delinococcus.
 NC SEQUENCE FROM N.A.
 NC STRAIN-RI:
 RX MEDLINE: 2003695.
 RX Nucleotide: 28655714.
 RA Dodson R.J., Hatt D.H., Oyam M.L., Nelson M.C., Richardson D.L.,
 McFate K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 Maleschewsky S., Grayson J., Kohnen J., Kohnen M., Flatschmann R.D.,
 RA Kohnen K.A., Nelson K.E., Salzberg S., Smith H.O., Ventur J.C.,
 "Genomic organization of the radioresistant bacterium Delinococcus
 radiodurans RI."
 RL Science 286:1571-1577(1999).
 DR TIGR: DR1160.
 DR INTERPRO: IPR02042.
 DR PFM: PF00233 GSD
 DR HHSR: PF00233 GSD
 SO SEQUENCE: 298 AA; 34332 MW; 100C79457DF6C6 Cnct4;

Query Match
 Query Local Similarity 85.7% Score 30; DB 2; Length 298;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 PROPOC 6
 DB 125 PROPOC 130